

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/557,288
Source: Pg 10
Date Processed by STIC: 11/28/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 11/28/2005

PATENT APPLICATION: US/10/557,288

TIME: 13:16:19

Input Set : A:\PTO.TS.txt

Output Set: N:\CRF4\11282005\J557288.raw

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3 <110> APPLICANT: ENEA-Ente per le Nuove Tecnologie e l'Ambiente
4     Consiglio Nazionale delle Ricerche
6 <120> TITLE OF INVENTION: Method for the preparation of transgenic plants
characterised by
7     Geminivirus lasting resistance
9 <130> FILE REFERENCE: PCT25622
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/557,288
C--> 12 <141> CURRENT FILING DATE: 2005-11-17
14 <150> PRIOR APPLICATION NUMBER: RM2003A000242
15 <151> PRIOR FILING DATE: 2003-05-19
17 <160> NUMBER OF SEQ ID NOS: 12
19 <170> SOFTWARE: PatentIn version 3.2
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 630
23 <212> TYPE: DNA
24 <213> ORGANISM: Geminivirus TYLCSV
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29 tgtgatttaa caaaagaaaa tgcactttcc caaataacaa acctacaaac acccaciaaac      120
31 aaattattca tcaaaatttg cagagaacta catgaaaatg gggaacctca tctccatatt      180
33 ctcacccaat tcgaaggaaa atacaattgt accaatcaac gattcttcga cctggtatcc      240
35 ccaaccaggt cagcacattt ccatccgaac attcagggag ctaaatcgag ctccgacgtc      300
37 aagtcctata tcgacaagga cggagatgtt cttgaatggg gtactttcca gatcgacgga      360
39 cgatctgcta ggggaggaca acagacagcc aacgacgctt acgcaaaggc aattaacgca      420
41 ggaagtaagt cgcaggctct tgatgtaatt aaagaattag cgcctagaga ttacgttcta      480
43 cattttcata atataaatag taatttagat aaggttttcc aggtgcctcc ggcaccttat      540
45 gtttctcctt ttttatcttc ttctttcgat caagttcctg atgaacttga aactggggtt      600
47 tccgagaacg tcatggatgc cgctgcgcgg      630
50 <210> SEQ ID NO: 2
51 <211> LENGTH: 630
52 <212> TYPE: DNA
53 <213> ORGANISM: Artificial
55 <220> FEATURE:
56 <223> OTHER INFORMATION: TYLCSV Rep-210 modified sequence
59 <220> FEATURE:
60 <221> NAME/KEY: CDS
61 <222> LOCATION: (1)..(630)
63 <400> SEQUENCE: 2
64 atg cct aga tcc gga agg ttt agc atc aaa gct aag aat tac ttc ttg      48
65 Met Pro Arg Ser Gly Arg Phe Ser Ile Lys Ala Lys Asn Tyr Phe Leu
66 1          5          10          15
68 aca tac ccc aag tgt gac tta act aag gag aat gca ttg tcc cag ata      96
69 Thr Tyr Pro Lys Cys Asp Leu Thr Lys Glu Asn Ala Leu Ser Gln Ile
70          20          25          30

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72 act aac ttg caa act ccc act aac aag ttg ttc att aag att tgt agg      144
73 Thr Asn Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg
74      35                        40                        45
76 gaa ctt cat gag aat gga gaa cca cat ctt cat atc ttg ata cag ttc      192
77 Glu Leu His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe
78      50                        55                        60
80 gaa ggc aag tat aac tgc acc aac caa cgt ttc ttt gac ctt gtg tcc      240
81 Glu Gly Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser
82 65      70                        75                        80
84 cct acc aga tca gcc cat ttt cat cca aac atc cag ggt gct aag tcg      288
85 Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser
86      85                        90                        95
88 agt tca gac gtg aag tca tac att gac aaa gac ggc gat gtg ctc gag      336
89 Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu
90      100                       105                       110
92 tgg gga act ttt cag ata gac ggt cga tcg gct aga gga ggt cag caa      384
93 Trp Gly Thr Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
94      115                       120                       125
96 aca gct aac gat gca tac gct aag gct atc aac gct gga tcc aag tca      432
97 Thr Ala Asn Asp Ala Tyr Ala Lys Ala Ile Asn Ala Gly Ser Lys Ser
98      130                       135                       140
100 cag gca ctt gac gta atc aaa gag tta gct cct agg gat tat gtt ctt      480
101 Gln Ala Leu Asp Val Ile Lys Glu Leu Ala Pro Arg Asp Tyr Val Leu
102 145      150                       155                       160
104 cat ttc cat aac atc aac agc aat ttg gac aaa gtg ttc caa gtg cca      528
105 His Phe His Asn Ile Asn Ser Asn Leu Asp Lys Val Phe Gln Val Pro
106      165                       170                       175
108 ccg gct cct tac gtt tca cct ttc tta agt tct tca ttt gat cag gtt      576
109 Pro Ala Pro Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asp Gln Val
110      180                       185                       190
112 cca gat gag ctt gag cat tgg gtg tcc gaa aac gtt atg gac gcc gca      624
113 Pro Asp Glu Leu Glu His Trp Val Ser Glu Asn Val Met Asp Ala Ala
114      195                       200                       205
116 gcg cgt      630
117 Ala Arg
118      210
121 <210> SEQ ID NO: 3
122 <211> LENGTH: 210
123 <212> TYPE: PRT
124 <213> ORGANISM: Artificial
126 <220> FEATURE:
127 <223> OTHER INFORMATION: Synthetic Construct
129 <400> SEQUENCE: 3
131 Met Pro Arg Ser Gly Arg Phe Ser Ile Lys Ala Lys Asn Tyr Phe Leu
132 1      5      10      15
135 Thr Tyr Pro Lys Cys Asp Leu Thr Lys Glu Asn Ala Leu Ser Gln Ile
136      20      25      30
139 Thr Asn Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg
140      35      40      45

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143 Glu Leu His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe
144      50                      55                      60
147 Glu Gly Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser
148 65                      70                      75                      80
151 Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser
152                      85                      90                      95
155 Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu
156                      100                     105                     110
159 Trp Gly Thr Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
160                      115                     120                     125
163 Thr Ala Asn Asp Ala Tyr Ala Lys Ala Ile Asn Ala Gly Ser Lys Ser
164                      130                     135                     140
167 Gln Ala Leu Asp Val Ile Lys Glu Leu Ala Pro Arg Asp Tyr Val Leu
168 145                      150                     155                     160
171 His Phe His Asn Ile Asn Ser Asn Leu Asp Lys Val Phe Gln Val Pro
172                      165                     170                     175
175 Pro Ala Pro Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asp Gln Val
176                      180                     185                     190
179 Pro Asp Glu Leu Glu His Trp Val Ser Glu Asn Val Met Asp Ala Ala
180                      195                     200                     205
183 Ala Arg
184      210
187 <210> SEQ ID NO: 4
188 <211> LENGTH: 630
189 <212> TYPE: DNA
190 <213> ORGANISM: Artificial
192 <220> FEATURE:
193 <223> OTHER INFORMATION: TYLCSV Rep-210 modified sequence
196 <220> FEATURE:
197 <221> NAME/KEY: CDS
198 <222> LOCATION: (1)..(630)
200 <400> SEQUENCE: 4
201 atg cct aga tcc gga agg ttt agc atc aaa gct aag aat tac ttc ttg      48
202 Met Pro Arg Ser Gly Arg Phe Ser Ile Lys Ala Lys Asn Tyr Phe Leu
203 1                      5                      10                      15
205 aca tac ccc aag tgt gac tta act aag gag aat gca ttg tcc cag ata      96
206 Thr Tyr Pro Lys Cys Asp Leu Thr Lys Glu Asn Ala Leu Ser Gln Ile
207                      20                      25                      30
209 act aac ttg caa act ccc act aac aag ttg ttc att aag att tgt agg      144
210 Thr Asn Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg
211                      35                      40                      45
213 gaa ctt cac gag aat gga gaa cca cat ctt cat atc ttg ata cag ttc      192
214 Glu Leu His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe
215      50                      55                      60
217 gaa ggc aag tat aac tgc acc aac caa cgt ttc ttt gac ctt gtg tcc      240
218 Glu Gly Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser
219 65                      70                      75                      80
221 cct acc aga tca gcc cat ttt cat cca aac atc cag ggt gct aag tcg      288
222 Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser

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223          85          90          95
225 agt tca gac gtg aag tca tac att gac aaa gac ggg gat gtg ctc gag      336
226 Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu
227          100          105          110
229 tgg gga act ttt cag ata gac ggt cga tcg gct aga gga ggt cag caa      384
230 Trp Gly Thr Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
231          115          120          125
233 aca gca aac gat gca tac gct aag gct atc aac gct gga tcc aag tca      432
234 Thr Ala Asn Asp Ala Tyr Ala Lys Ala Ile Asn Ala Gly Ser Lys Ser
235          130          135          140
237 cag gca ctt gac gta atc aaa gag tta gct cct agg gat tat gtt ctt      480
238 Gln Ala Leu Asp Val Ile Lys Glu Leu Ala Pro Arg Asp Tyr Val Leu
239 145          150          155          160
241 cat ttc cat aac atc aac agc aat ttg gac aaa gtg ttc caa gtg cca      528
242 His Phe His Asn Ile Asn Ser Asn Leu Asp Lys Val Phe Gln Val Pro
243          165          170          175
245 ccg gct cct tac gtt tca cct ttc tta agt tct tca ttt gat cag gtt      576
246 Pro Ala Pro Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asp Gln Val
247          180          185          190
249 cca gat gag ctt gag cat tgg gtg tct gaa aac gtt atg gac gcc gca      624
250 Pro Asp Glu Leu Glu His Trp Val Ser Glu Asn Val Met Asp Ala Ala
251          195          200          205
253 gcc cgt      630
254 Ala Arg
255          210
258 <210> SEQ ID NO: 5
259 <211> LENGTH: 210
260 <212> TYPE: PRT
261 <213> ORGANISM: Artificial
263 <220> FEATURE:
264 <223> OTHER INFORMATION: Synthetic Construct
266 <400> SEQUENCE: 5
268 Met Pro Arg Ser Gly Arg Phe Ser Ile Lys Ala Lys Asn Tyr Phe Leu
269 1          5          10          15
272 Thr Tyr Pro Lys Cys Asp Leu Thr Lys Glu Asn Ala Leu Ser Gln Ile
273          20          25          30
276 Thr Asn Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg
277          35          40          45
280 Glu Leu His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe
281          50          55          60
284 Glu Gly Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser
285 65          70          75          80
288 Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser
289          85          90          95
292 Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu
293          100          105          110
296 Trp Gly Thr Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
297          115          120          125
300 Thr Ala Asn Asp Ala Tyr Ala Lys Ala Ile Asn Ala Gly Ser Lys Ser

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301      130      135      140
304 Gln Ala Leu Asp Val Ile Lys Glu Leu Ala Pro Arg Asp Tyr Val Leu
305 145      150      155      160
308 His Phe His Asn Ile Asn Ser Asn Leu Asp Lys Val Phe Gln Val Pro
309      165      170      175
312 Pro Ala Pro Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asp Gln Val
313      180      185      190
316 Pro Asp Glu Leu Glu His Trp Val Ser Glu Asn Val Met Asp Ala Ala
317      195      200      205
320 Ala Arg
321      210
324 <210> SEQ ID NO: 6
325 <211> LENGTH: 774
326 <212> TYPE: DNA
327 <213> ORGANISM: Artificial
329 <220> FEATURE:
330 <223> OTHER INFORMATION: TYLCSV Coat Protein modified sequence
333 <220> FEATURE:
334 <221> NAME/KEY: CDS
335 <222> LOCATION: (1)..(774)
337 <400> SEQUENCE: 6
338 atg cca aag aga act ggt gat att cta atc tca act ccc gtg tct aag      48
339 Met Pro Lys Arg Thr Gly Asp Ile Leu Ile Ser Thr Pro Val Ser Lys
340 1      5      10      15
342 gtg cgt agg aga ctt aac ttt gac tct ccg tac acc tct cgt gca gct      96
343 Val Arg Arg Arg Leu Asn Phe Asp Ser Pro Tyr Thr Ser Arg Ala Ala
344      20      25      30
346 gct ccc aca gtc cag ggc att aag agg cga tct tgg aca tac aga cct      144
347 Ala Pro Thr Val Gln Gly Ile Lys Arg Arg Ser Trp Thr Tyr Arg Pro
348      35      40      45
350 atg tac agg aaa ccg agg atg tat agg atg tat cgt agc cca gat gtg      192
351 Met Tyr Arg Lys Pro Arg Met Tyr Arg Met Tyr Arg Ser Pro Asp Val
352 50      55      60
354 cct cct ggt tgc gaa gga ccc tgc aag gtg caa tcg tat gag caa cgt      240
355 Pro Pro Gly Cys Glu Gly Pro Cys Lys Val Gln Ser Tyr Glu Gln Arg
356 65      70      75      80
358 gac gat gtg aag cac acc gga gtt gtt cgt tgc gtt tct gat gtg act      288
359 Asp Asp Val Lys His Thr Gly Val Val Arg Cys Val Ser Asp Val Thr
360      85      90      95
362 aga ggt tca ggt atc act cac agg gtg gga aag cgt ttc tgt att aag      336
363 Arg Gly Ser Gly Ile Thr His Arg Val Gly Lys Arg Phe Cys Ile Lys
364      100      105      110
366 tct att tac ata ttg ggt aag atc tgg atg gac gag aat atc aag aaa      384
367 Ser Ile Tyr Ile Leu Gly Lys Ile Trp Met Asp Glu Asn Ile Lys Lys
368      115      120      125
370 cag aat cac act aat cag gtt atg ttc ttt ctt gtg cga gat cga aga      432
371 Gln Asn His Thr Asn Gln Val Met Phe Phe Leu Val Arg Asp Arg Arg
372      130      135      140
374 cca tac gga acc agc cca atg gac ttc ggc cag gtg ttt aat atg ttc      480

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/557,288

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Input Set : A:\PTO.TS.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:2,3,4,5,6,7,8,9,10,11

VERIFICATION SUMMARY

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Input Set : A:\PTO.TS.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date